

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Tobin, James

(ii) TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genetics Institute, Inc.  
(B) STREET: 87 Cambridgepark Drive  
(C) CITY: Cambridge  
(D) STATE: MA  
(E) COUNTRY: USA  
(F) ZIP: 02140

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: Patentin Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Brown, Scott A.  
(B) REGISTRATION NUMBER: 32,724  
(C) REFERENCE/DOCKET NUMBER: GI5252

(viii) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (617) 499-8224  
(B) TELEFAX: (617) 876-5851

## T02030 "BEC33650"

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2456 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (iii) HYPOTHETICAL: NO

## (iv) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 734..1999

## (v) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCGCCACCC	CCAGGCTCTG	GCAGCACCA	GGCCATGCA	AGCTGCTTAA	CTTACATAGCC	60
CCAGCCTCA	CCCTAGCCC	ATTCGAGTTC	ACAAACTGA	GACCAACGAA	GTGTCAAAGAG	120
CCAGGCCAG	CTGAGTGGCC	CAAGTACCA	GACCAAGAG	CGAGGTTAG	GCAGAAAGCC	180
TGGCAGCAG	GGCAGGGTG	GGCCTAGGG	TGGAGATGCA	GGATGGGTC	AGATCCTTA	240
TGACACCTT	CCCCCAGGT	GATAGCTT	GCCTAGTTA	ATCAGAGGCA	GTGATAAGCC	300
CTGGACCAAG	TGGGGTAAA	TACCAAGAT	CCCAACAGCT	GGACTGGAGG	GGTTAAATGGG	360
AGTGCTGAG	CTGGTNSCAG	TGCTTGTGTC	CAGGGTGG	CCCAAGGGC	AGTGGAGGGG	420
GAGTTGGTGG	CAACAGTCGT	TGCTTGTGCG	TTCGGTTCG	CCGGGAAAGC	CCAGGGAGTC	480
GATGGAGGGT	GTGAGGGGT	GTGTTGTGTC	GTGTTGTGTT	GTGCGCGGCG	GTGCGCGGCG	540
ACGCACTOC	AAAGGACTCG	GTATAGTGS	GGAAAGGGAA	CTTCAGGGTCA	GTTCGGCGAG	600

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TTGATTCCTA CAGCTTACCCACTCTTCA	720
AGAGGCGAGC TTCTAGCTCC CATTCTACGG	769
GGGGGAAATT TTGAGGCTCTA	817
CCCTCTCCCCA CAG ATG AGC AGC AGC TGC TCA GGG CTG AGC AGG GTC CTC	865
Met Ser Ser Cys Ser Gly Leu Ser Arg Val Leu	
1 5	
15 20	
25	
GTG GCC GTG GCT ACA GCC CTCG GTG TCT GGC TCC TCC CCC TGC CCC CAG	913
Val Ala Val Ala Thr Ala Leu Val Ser Ala Ser Pro Cys Pro Gln	
GGCC TGG CCC CCA GGG GTC CAG TAT GGG CAG CCA GGC AGG TCC GTC	
Ala Val Trp Gly Pro Pro Gln Tyr Gln Gln Pro Gln Arg Ser Val	
30 35	
40	
GTG TGT CCT GGA GTG ACT GCC GGG GAC CCA GTG TCC TGG TTT	
Leu Cys Pro Gln Val Thr Ala Gln Asp Pro Val Ser Trp Phe	
45 50	
55	
GGG GAG CCA AAG CTC CAG GGA CCT GAC TGT GGG CTA GGG	961
Arg Asp Gly Lys Leu Leu Gln Gln Pro Asp Ser Gln Leu Gln	
60 65	
70 75	
GAT GTC CTC CAG GCA GAC AGC ACT GAT GAG GGC ACC TAC	1009
His1 Gln Leu Val Leu Ala Asp Ser Thr Asp Gln Gly Thr Tyr	
95 100	
105 110	
TGC CAG ACC CTC GAT GGT GCA CTT GGG GGC ACA GTG ACC CTC	1057
Leu Cys Gln Thr Leu Asp Gln Ala Leu Gln Gln Thr Val Thr Leu Gln	
CCG TAC CCT CCA GGC CGC CCT GTC TCC TCC CAA GCA GCC GAC	1105
Gly Tyr Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp	
115 120	
125 130	
135 140	
GAC AAC TTC TCT TGC ACT TGG AGT CCC AGC CAG ATC AGC GGT TPA	1153
Glu Asn Phe Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gln Ile	

CCC ACC CGC TAC CTC ACC TCC TAC AGG AGG AGA GTC CTA GGA GCT	1201
Pro Thr Arg Tyr Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Glu Ala	
145 150 155	
GAT AGC CGG AGG AGG AGT CCA TCC ACA GGG CCC TGG CCA TGC CCA CAG	1249
Asp Ser Gln Arg Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln	
160 165 170	
GAT CCC CTA GGG GCT GCC CGC TGT GTC CAC GGG GCT GAG TTC TGG	1297
Asp Pro Leu Gly Ala Ala Arg Cys Val His Glu Ala Glu Phe Trp	
175 180 185	
AGC CAG TAC CGG ATT AAT GTG ACT GAG GTG AAC CCA CTT GGT GCC AGC	1345
Ser Gln Tyr Arg Ile Asn Val Thr Glu Val Asn Pro Leu Glu Ala Ser	
190 195 200	
ACA CGC CTTG GAT GNG AGC TTTG CAG AGC ATC TTT CGC CCT GAC CCA	1393
Thr Arg Leu Leu Asp Val Ser Leu Glu Ser Ile Leu Arg Pro Asp Pro	
205 210 215 220	
CCC CAG GCC CTG CGG GPA GAG TCA GPA CCA GGT TAC CCC CGA CGC CTG	1441
Pro Gln Glu Leu Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Arg Leu	
225 230 235	
CGA GCC AGC TGG ACA TAC CCT GCC TCC TGG CCG CAG CAT CCA GCC CAC TTC	1489
Arg Ala Ser Trp Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe	
240 245 250	
CTG CTC AAG TTC CGT TTG CAG TAC CGT CCG GCG CAG CAT CCA GCC TGG	1537
Leu Leu Lys Phe Arg Leu Glu Tyr Arg Pro Ala Glu His Pro Ala Trp	
255 260 265	
TCC ACG GNG GAG CCA GCT GGA CTT GAG GAG GTG ATC ACA GAT GCT GTG	1585
Ser Thr Val Glu Pro Ala Gly Leu Glu Val Ile Thr Asp Ala Val	
270 275 280	
GCT GGG CTG CCC CAT GCT GTA CGA GTC AGT GCC CGG GAC TTT CTA GAT	1633
Ala Gly Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp	
285 290 295 300	

GCT GGC ACC TGG AGC ACC TGG AGC CGG GAG GCA ACT CGG AGC  
 Ala Gly Thr Trp Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser 1681  
 305 310 315  
 ACT GGG ACC ATA CCA AAG GAG ATA CCA GCA TGG GEC CTA CAC ACG  
 Thr Gly Thr Ile Pro Lys Glu Ile Pro Ala Trp Gly Glu Leu His Thr 1729  
 320 325 330  
 CAG CCA GAG CTC GAG CCT CAG GTG GAC AGC CCT GCT CCT CCA AGG CCC  
 Gln Pro Glu Val Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro 1777  
 335 340 345  
 TCC CTC CAA CCA CAC CCT CGG CTA CTT GAT CAC AGG GAC TCT GTG GAG  
 Ser Leu Gln Pro His Pro Arg Leu Asp His Arg Asp Ser Val Glu 1825  
 350 355 360  
 CAG GTA GCT GNG CTC GCG TCT TGT GGA ATC CTT TCT TGT CTC GGA CTG  
 Gln Val Ala Val Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu 1873  
 365 370 375 380  
 GTC GCT GGG GGC CTC GCA CTC GGG CTC TCG AGG CTC AGA CGC CGT  
 Val Ala Gly Ala Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Arg Gly 1921  
 385 390 395  
 GGG AAG GAT GGA TCC CCA AAG CCT GGG RTC TGT GCC TCA GTG ATT CCA  
 Gly Lys Asp Gly Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Thr Pro 1969  
 400 405 410  
 CNG GAC AGG CGT CCA GGA GCT CCA AAC CNG TAGAGGCC AGGGGCTT  
 Val Asp Arg Arg Pro Gly Ala Pro Asn Leu 2019  
 415 420  
 CGCCAGATTC CACCTATAAT TCTGTCCTTCG TGTTGTTGGAT GGATGGACAG ATAGAAACCA  
 CGCAGGAGAG TAGATGCCTA TGGTTGGATTC TCAAGCTGAA GTCAGCTGTTG GAGGCCATTT 2079  
 2139  
 CTGTGAGAC CTGTATTTCA AATTGGCAGC TCAAAAGTGC TTGTACCTCT GATTTCACCC  
 CAGAGTNGA GTCCTGCTCA AGGAACGTGT GTAATGCTTA CTCCTGTCGTC CAGTGTGAC 2199  
 2259

AGTCTGTCG	TGAGCAGGG	AAATGTTATT	CTCTCATGC	ATGATCTGAG	GTGCTGGGG	2319
AGTGTGTCG	GGTCTCTGCG	TCTTGCCATT	TCCCTTGCA	GGGGTGTCG	AGGGTGAAAT	2379
AAAGAGAAATA	AGGAAAGTCT	TGGAGATATT	ACTAGAAGAA	AAAAAAA	AGTCGACCGG	2439
						2456

### 13) INFORMATION EOB SEQ ID NO: 2:

EVIDENCE FOR ACCEPTANCE.

(1) SEQUENCE CHARACTERISTICS:

114 115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:									
Ser Ser Cys Ser Gly Leu Ser Arg Val Leu Val Ala Val Ala									
1	5	10	15						
Thr Ala Leu Val Ser Ala Ser Ser Pro Cys Pro Gln Ala	Trp								
20	25	30							
Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Ser Val Lys	Leu	Cys							
35	40	45							
Pro Gly Val Thr Ala Gly Asp Pro Val Ser Trp Phe Arg	Asp	Gly							
50	55	60							
Pro Lys Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His	Glu	Leu	Val						
65	70	75	80						
Leu Ala Gln Ala Asp Ser Thr Asp Glu Gly Thr Tyr Ile	Cys	Gln	Thr						
85	90	95	100						
Leu Asp Gly Ala Leu Gly Gly Thr Val Thr Leu Gln Leu	Gly	Tyr	Pro						
100	105	110							

Pro Ala Arg Pro Val Val Ser Cys Gln Ala Ala Asp Tyr Glu Asn Phe  
 115 120  
 Ser Cys Thr Trp Ser Pro Ser Gln Ile Ser Gly Leu Pro Thr Arg Tyr  
 130 135  
 Leu Thr Ser Tyr Arg Lys Lys Thr Val Leu Gly Ala Asp Ser Gln Arg  
 145 150  
 Arg Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro Leu Gly  
 165 170  
 Ala Ala Arg Cys Val Val His Gly Ala Glu Phe Trp Ser Gln Tyr Arg  
 180 185  
 Ile Asn Val Thr Glu Val Asn Pro Leu Gly Ala Ser Thr Arg Leu Leu  
 195 200  
 Asp Val Ser Leu Gln Ser Ile Leu Arg Pro Asp Pro Pro Gln Gly Leu  
 210 215  
 Arg Val Glu Ser Val Pro Gly Tyr Pro Arg Leu Arg Ala Ser Trp  
 225 230  
 Thr Tyr Pro Ala Ser Trp Pro Cys Gln Pro His Phe Leu Leu Lys Phe  
 245 250  
 Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Trp Ser Thr Val Glu  
 260 265  
 Pro Ala Gly Leu Glu Glu Val Ile Thr Asp Ala Val Ala Gly Leu Pro  
 275 280  
 His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly Thr Trp  
 290 295  
 Ser Thr Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Gly Thr Ile  
 305 310  
 Pro Lys Glu Ile Pro Ala Trp Gly Gln Leu His Thr Gln Pro Glu Val

325	330	335
Glu Pro Gln Val Asp Ser Pro Ala Pro Pro Arg Pro Ser Leu Gln Pro		
340	345	350
His Pro Arg Leu Leu Asp His Arg Asp Ser Val Glu Gln Val Ala Val		
355	360	365
Leu Ala Ser Leu Gly Ile Leu Ser Phe Leu Gly Leu Val Ala Gly Ala		
370	375	380
Leu Ala Leu Gly Leu Trp Leu Arg Leu Arg Gly Gly Lys Asp Gly		
385	390	395
Ser Pro Lys Pro Gly Phe Leu Ala Ser Val Ile Pro Val Asp Arg Arg		
405	410	415
Pro Gly Ala Pro Asn Leu		
420		

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1714 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO

- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 34..1359
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTCCTAGCC	GATGGAGGA	AGTCCTGGAGC	CTG GCA CTC AGT CAC TGT GAT	54
	Met Ala	Leu Ser His Cys Asp		
1				
TAT CAA GAT GAG CAG CAG CTC AGG GCT GAC CAG GGT CCT GGT GCG GGC				102
Tyr Gln Asp Glu Gln Gln Leu Arg Ala Asp Gln Gly Pro Gly Gly	10	15	20	
CGT GCT Aca Gcc Ctg Ctg Gng Tct Tcc Tcc Ccc Tsc Ccc Caa Gct Tgg				150
Arg Ala Thr Ala Leu Val Ser Ser Ser Pro Gln Ala Trp	25	30	35	
GTC CCT CCA GGG GTC CAG TAT GGA CAA CCT GGC AGG CCC GNG TNG CTG				198
Gly Pro Pro Gly Val Gln Tyr Gly Gln Pro Gly Arg Pro Val Met Leu	40	45	50	55
TGC TGC CCC GGA GTG Act GCT GGG ACT CCA Gtg Tcc Tgg Ttt Ctg GAT				246
Cys Cys Pro Gly Val Ser Ala Gly Thr Pro Val Ser Trp Phe Arg Asp	60	65	70	
GGA GAT TAA AGG CTG CTC CAG GGA CCT GAC TCT GGC TTA GGA CTC AGA				294
Gly Asp Ser Arg Leu Leu Gln Gly Pro Asp Ser Gly Leu Gly His Arg	75	80	85	
CTG GTC Ttg GCC CAG Gng GAC NGC CCT CAT GAA GGC ACT TAT GTC Tgc				342
Leu Val Leu Ala Gln Val Asp Ser Pro Asp Glu Gly Thr Tyr Val Cys	90	95	100	
CAG ACC CTG GAT GGT Gta Tca GGG GGC ATG GTG ACC CTG AAG CTG GGC				390
Gln Thr Leu Asp Gly Val Ser Gly Gly Met Val Thr Leu Lys Leu Gly	105	110	115	
Ttt CCC CCA GCA CGT CCT GAA GTC TCC TGC CAA GCG GTA GAC TAT GAA				438
Phe Pro Pro Ala Arg Pro Glu Val Ser Cys Gln Ala Val Asp Tyr Glu	120	125	130	135
AAC TTC TCC TGT ACT Tgs AGT CCA GGC CAG GTC AGC GGT TTG CCC ACC				486
Asn Phe Ser Cys Thr Trp Ser Pro Gly Gln Val Ser Gly Leu Pro Thr	140	145	150	

CGC TAC CTT ACT TCC TAC AGG AAG AAG ACG CTC CCA GGA CCT GAG AGT  
 Arg Tyr Leu Thr Ser Tyr Arg Lys Pro Thr Leu Pro Gly Ala Glu Ser  
 155 160 165  
 534  
 CAG AGG GAA AGT CCA TCC ACC GGG CCT TGG CCG TGT CCA CGG GAC CCT  
 Gln Arg Gln Ser Pro Ser Thr Gly Pro Trp Pro Cys Pro Gln Asp Pro  
 170 175 180  
 582  
 CTG GAG GCC TCC CGA TGT GTC GTC GTC CAT GGG GCA GAG TTC TGG AGT GAG  
 Leu Glu Ala Ser Arg Cys Val His Gly Ala Glu Phe Thr Ser Glu  
 185 190 195  
 630  
 TAC CGG ATC AAT GTC ACC GAG GTC AAC GAC CGT GGC AGC ACG TGC  
 Tyr Arg Ile Asn Val Thr Val His Gly Ala Ser Thr Cys  
 200 205 210  
 678  
 CTA CTG GAT GTG AGA TTA CAG AGC ATC TTG CGT CCT GAT CCA CCC CAA  
 Leu Leu Asp Val Arg Leu Gln Ser Ile Leu Arg Pro Asp Pro Gln  
 220 225  
 726  
 GGA CTG CGG GTG GAA TCC GTC GTC CCA CGT TAC CGG AGA CGC CTC GAT GCC  
 Gly Leu Arg Val Glu Ser Val Pro GLY Tyr Pro Arg Arg Leu His Ala  
 235 240 245  
 774  
 AGC TGG ACA TAC CCT GCC TCC TCG CGT CGC CAA CCC CAC TTT CTG CTC  
 Ser Thr Tyr Pro Ala Ser Thr Arg Arg Gln Pro His Leu Leu  
 250 255  
 822  
 AAG TTC CGG TTG CAA TAC CGA CGA CCA CAG CAT CCA CGC TGG TCC ACG  
 Lys Phe Arg Leu Gln Tyr Arg Pro Ala Gln His Pro Ala Thr Ser Thr  
 265 270  
 870  
 GTG GAG CCC ATT GGC TTG GAG GAA GTG ATA ACA GAT GCT GTG GCT GGG  
 Val Glu Pro Ile Gly Ile Glu Glu Val Ile Thr Asp Ala Val Ala Gly  
 280 285  
 918  
 CTG CCA CAC GAC GCG GTC CGA CGA GTC AGT GCC AGG GAC TTT CTG GAT GCT GGC  
 Leu Pro His Ala Val Arg Val Ser Ala Arg Asp Phe Leu Asp Ala Gly  
 300 305  
 966

ACC TGG AGC GCC TGG AGC CCA GAG TGG GGT ACT AGC ACT GCT	1014
Thr Trp Ser Ala Trp Ser Pro Glu Ala Trp Gly Thr Pro Ser Thr Glu	320
315	325
CCC CTG CAG GAT GAG ATA CCT GAT TGG AGC CAG GGA CAT GGA CAG CAG	1062
Pro Leu Gln Asp Glu Ile Pro Asp Trp Ser Glu Gly His Gly Gln Gln	330
335	340
CTA GAG GCA GTC GCA GCT CAG GAC AGC CCG GCT GCA AGG CCT	1110
Leu Glu Ala Val Ala Gln Glu Asp Ser Pro Ala Pro Ala Arg Pro	345
350	355
TCC T <sup>r</sup> G CAG CCG GAC CCA AGG CCA CTT GAT CAC AGG GAC CCC T <sup>r</sup> G GAG	1158
Ser Leu Gln Pro Asp Pro Arg Pro Leu Asp His Arg Asp Pro Leu Glu	360
365	370
375	375
CAA GTA GCT GNG TTA GCG TCT CTC GGA ATC TTC TCT TGC CTT GGC CTC	1206
Gln Val Ala Val Leu Ala Ser Leu Gly Ile Phe Ser Cys Leu Gly Ieu	380
385	390
GCT GTT GGA GCT CTG GCA CTG GGG CTC TGG CTG AGG CTC AGA CGG AGT	1254
Ala Val Gly Ala Leu Ala Leu Gly Ieu Trp Leu Arg Leu Arg Arg Ser	395
400	405
GGS AAG GAT GGA CGG CAA AAA CCT GGG CTC TGT GCA CCC ATG ATC CCG	1302
Gly Lys Asp Gly Pro Glu Lys Pro Glu Leu Leu Ala Pro Met Ile Pro	410
415	420
GTC GAA AGG CTT CCA GGA ATT CCA AAC CTC CAG AGG ACC CCA GAG AAC	1350
Val Glu Lys Leu Pro Gly Ile Pro Asn Leu Gln Arg Thr Pro Glu Asn	425
430	435
TTC AGC TGTATTCTTCAG TGTAAACCGG TCAAGACTGG GGTGTAAAG AGGACAGGCA	1406
Phe Ser	440
GAAAGGGCG GGGCAGTGGAA TCCCTGTGGA TGGAGGTCTC AGCTGAAGT <sup>r</sup> CTGAGCTCTT	1466
TTCCTTGACCA CCTPATACCTCC AAACCTTGCTG CGCGCTGAGA CTTCGGATGT	1526

CCTGAGCTGG AAGTCCACCT GAGGAATGCG TACAGAATGCT TGTGTTCCG TGTAGCTGNG 1586  
 TGTATGAG AGAGGGAGCA AAAGTCTCT GCAGATGTGT AGAGATGTTT GGAGAGTG 1646  
 TGCCTGCTTG GCCTTGCGCC TTCTGGGAG TGCTGAAGGT TGAAATAAA GAGACGGAG 1706  
 TTTTTGGA. 1714

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Leu Ser His Cys Asp Tyr Glu Asp Glu Gln Leu Leu Arg	1
5	10
Ala Asp Gln Gly Pro Gly Arg Ala Thr Ala Leu Val Ser Ser Ser	15
20	25
Ser Pro Cys Pro Gln Ala Trp Gly Pro Pro Gly Val Gln Tyr Gly Gln	30
35	40
Pro Gly Arg Pro Val Met Leu Cys Cys Pro Gly Val Ser Ala Gly Thr	45
50	55
Pro Val Ser Trp Phe Arg Asp Gly Asp Ser Arg Leu Leu Gln Gly Pro	60
65	70
Asp Ser Gly Leu Gly His Arg Leu Val Leu Ala Gln Val Asp Ser Pro	75
85	90
Asp Glu Gly Thr Tyr Val Cys Gln Thr Leu Asp Gly Val Ser Gly Gln	95
100	105
110	



Ser	Gln	Gly	His	Gly	Gln	Gln	Leu	Ala	Val	Ala	Gln	Glu	Asp		
325													335		
Ser	Pro	Ala	Pro	Ala	Arg	Pro	Ser	Leu	Gln	Pro	Asp	Pro	Arg	Pro	Leu
340															350
Asp	His	Arg	Asp	Pro	Leu	Glu	Gln	Val	Ala	Val	Leu	Ala	Ser	Leu	Gly
355															365
Ile	Phe	Ser	Cys	Leu	Gly	Leu	Ala	Val	Gly	Ala	Leu	Ala	Leu	Gly	Leu
370															380
Ile	Phe	Ser	Cys	Leu	Gly	Leu	Ala	Val	Gly	Ala	Leu	Ala	Leu	Gly	Leu
385															395
Trp	Leu	Arg	Leu	Arg	Arg	Ser	Gly	Lys	Asp	Gly	Pro	Gln	Lys	Pro	Gly
405															415
Leu	Leu	Ala	Pro	Met	Ile	Pro	Val	Glu	Lys	Leu	Pro	Gly	Ile	Pro	Asn
420															430
Leu	Gln	Arg	Thr	Pro	Glu	Asn	Phe	Ser							
435															440